



#7

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## SEQUENCE LISTING

<110> Boehringer Ingelheim International GmbH

<120> Method for identifying compounds that modulate sister chromatid separation

<130> 0652.2290001

<140> To be assigned

<141> Herewith

<150> EP 01 101 252.3

<151> 2001-01-19

<150> US 60/297,440

<151> 2001-06-13

<160> 12

<170> PatentIn Ver. 2.1

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<211> 6668

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ggg ctg agc ctt cag gag atg cct gga gat gtc ccc ctg gcc cgc atc Gly Leu Ser Leu Gln Glu Met Pro Gly Asp Val Pro Leu Ala Arg Ile 1660 1665 1670	5163
cag cgc ctc ttt tcc ttc agg gct ttg gaa tct ggc cac ttc ccc cag Gln Arg Leu Phe Ser Phe Arg Ala Leu Glu Ser Gly His Phe Pro Gln 1675 1680 1685	5211
cct gaa aag gag agt ttc cag gag cgc ctg gct ctg atc ccc agt ggg Pro Glu Lys Glu Ser Phe Gln Glu Arg Leu Ala Leu Ile Pro Ser Gly 1690 1695 1700 1705	5259
gtg act gtg tgt gtg ttg gcc ctg gcc acc ctc cag ccc gga acc gtg Val Thr Val Cys Val Leu Ala Leu Ala Thr Leu Gln Pro Gly Thr Val 1710 1715 1720	5307
ggc aac acc ctc ctg ctg acc cgg ctg gaa aag gac agt ccc cca gtc Gly Asn Thr Leu Leu Thr Arg Leu Glu Lys Asp Ser Pro Pro Val 1725 1730 1735	5355
agt gtg cag att ccc act ggc cag aac aag ctt cat ctg cgt tca gtc Ser Val Gln Ile Pro Thr Gly Gln Asn Lys Leu His Leu Arg Ser Val 1740 1745 1750	5403
ctg aat gag ttt gat gcc atc cag aag gca cag aaa gag aac agc agc Leu Asn Glu Phe Asp Ala Ile Gln Lys Ala Gln Lys Glu Asn Ser Ser 1755 1760 1765	5451
tgt act gac aag cga gaa tgg tgg aca ggg cgg ctg gca ctg gac cac Cys Thr Asp Lys Arg Glu Trp Trp Thr Gly Arg Leu Ala Leu Asp His 1770 1775 1780 1785	5499
agg atg gag gtt ctc atc gct tcc cta gag aag tct gtg ctg ggc tgc Arg Met Glu Val Leu Ile Ala Ser Leu Glu Lys Ser Val Leu Gly Cys 1790 1795 1800	5547



tgg aag ggg ctg ctg ctg ccg tcc agt gag gag ccc ggc cct gcc cag	5595
Trp Lys Gly Leu Leu Leu Pro Ser Ser Glu Glu Pro Gly Pro Ala Gln	
1805 1810 1815	
gag gcc tcc cgc cta cag gag ctg cta cag gac tgt ggc tgg aaa tat	5643
Glu Ala Ser Arg Leu Gln Glu Leu Leu Gln Asp Cys Gly Trp Lys Tyr	
1820 1825 1830	
cct gac cgc act ctg ctg aaa atc atg ctc agt ggt gcc ggt gcc ctc	5691
Pro Asp Arg Thr Leu Leu Lys Ile Met Leu Ser Gly Ala Gly Ala Leu	
1835 1840 1845	
acc cct cag gac att cag gcc ctg gcc tac ggg ctg tgc cca acc cag	5739
Thr Pro Gln Asp Ile Gln Ala Leu Ala Tyr Gly Leu Cys Pro Thr Gln	
1850 1855 1860 1865	
cca gag cga gcc cag gag ctc ctg aat gag gca gta gga cgt cta cag	5787
Pro Glu Arg Ala Gln Glu Leu Leu Asn Glu Ala Val Gly Arg Leu Gln	
1870 1875 1880	
ggc ctg aca gta cca agc aat agc cac ctt gtc ttg gtc cta gac aag	5835
Gly Leu Thr Val Pro Ser Asn Ser His Leu Val Leu Val Leu Asp Lys	
1885 1890 1895	
gac ttg cag aag ctg ccg tgg gaa agc atg ccc agc ctc caa gca ctg	5883
Asp Leu Gln Lys Leu Pro Trp Glu Ser Met Pro Ser Leu Gln Ala Leu	
1900 1905 1910	
cct gtc acc cgg ctg ccc tcc ttc cgc ttc cta ctc agc tac tcc atc	5931
Pro Val Thr Arg Leu Pro Ser Phe Arg Phe Leu Leu Ser Tyr Ser Ile	
1915 1920 1925	
atc aaa gag tat ggg gcc tcg cca gtg ctg agt caa ggg gtg gat cca	5979
Ile Lys Glu Tyr Gly Ala Ser Pro Val Leu Ser Gln Gly Val Asp Pro	
1930 1935 1940 1945	
cga agt acc ttc tat gtc ctg aac cct cac aat aac ctg tca agc aca	6027
Arg Ser Thr Phe Tyr Val Leu Asn Pro His Asn Asn Leu Ser Ser Thr	
1950 1955 1960	
gag gag caa ttt cga gcc aat ttc agc agt gaa gct ggc tgg aga gga	6075
Glu Glu Gln Phe Arg Ala Asn Phe Ser Ser Glu Ala Gly Trp Arg Gly	
1965 1970 1975	
gtg gtt ggg gag gtg cca aga cct gaa cag gtg cag gaa gcc ctg aca	6123
Val Val Gly Glu Val Pro Arg Pro Glu Gln Val Gln Glu Ala Leu Thr	
1980 1985 1990	
aag cat gat ttg tat atc tat gca ggg cat ggg gct ggt gcc cgc ttc	6171
Lys His Asp Leu Tyr Ile Tyr Ala Gly His Gly Ala Gly Ala Arg Phe	
1995 2000 2005	
ctt gat ggg cag gct gtc ctg cgg ctg agc tgt cgg gca gtg gcc ctg	6219
Leu Asp Gly Gln Ala Val Leu Arg Leu Ser Cys Arg Ala Val Ala Leu	
2010 2015 2020 2025	
ctg ttt ggc tgt agc agt gcg gcc ctg gct gtg cat gga aac ctg gag	6267
Leu Phe Gly Cys Ser Ser Ala Ala Leu Ala Val His Gly Asn Leu Glu	
2030 2035 2040	
ggg gct ggc atc gtg ctc aag tac atc atg gct ggt tgc ccc ttg ttt	6315
Gly Ala Gly Ile Val Leu Lys Tyr Ile Met Ala Gly Cys Pro Leu Phe	

2045	2050	2055	
ctg ggt aat ctc tgg gat gtg act gac cgc gac att gac cgc tac acg			6363
Leu Gly Asn Leu Trp Asp Val Thr Asp Arg Asp Ile Asp Arg Tyr Thr			
2060	2065	2070	
gaa gct ctg ctg caa ggc tgg ctt gga gca ggc cca ggg gcc ccc ctt			6411
Glu Ala Leu Leu Gln Gly Trp Leu Gly Ala Gly Pro Gly Ala Pro Leu			
2075	2080	2085	
ctc tac tat gta aac cag gcc cgc caa gct ccc cga ctc aag tat ctt			6459
Leu Tyr Tyr Val Asn Gln Ala Arg Gln Ala Pro Arg Leu Lys Tyr Leu			
2090	2095	2100	2105
att ggg gct gca cct ata gcc tat ggc ttg cct gtc tct ctg cgg taa			6507
Ile Gly Ala Ala Pro Ile Ala Tyr Gly Leu Pro Val Ser Leu Arg			
2110	2115	2120	
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atttaatcct taggataact cttttaaagt gattttcccc agtgttttat atgaaacatt			6627
tccttttgat ttaacctcag tataataaag atacatcatt t			6668
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Lys Glu Ala Glu Glu Leu Leu Pro Asp Leu Lys Glu Phe Leu Ser Asn			
20	25	30	
Pro Pro Ala Gly Phe Pro Ser Ser Arg Ser Asp Ala Glu Arg Arg Gln			
35	40	45	
Ala Cys Asp Ala Ile Leu Arg Ala Cys Asn Gln Gln Leu Thr Ala Lys			
50	55	60	
Leu Ala Cys Pro Arg His Leu Gly Ser Leu Leu Glu Leu Ala Glu Leu			
65	70	75	80
Ala Cys Asp Gly Tyr Leu Val Ser Thr Pro Gln Arg Pro Pro Leu Tyr			
85	90	95	
Leu Glu Arg Ile Leu Phe Val Leu Leu Arg Asn Ala Ala Ala Gln Gly			
100	105	110	
Ser Pro Glu Val Thr Leu Arg Leu Ala Gln Pro Leu His Ala Cys Leu			
115	120	125	
Val Gln Cys Ser Arg Glu Ala Ala Pro Gln Asp Tyr Glu Ala Val Ala			
130	135	140	
Arg Gly Ser Phe Ser Leu Leu Trp Lys Gly Ala Glu Ala Leu Leu Glu			
145	150	155	160
Arg Arg Ala Ala Phe Ala Ala Arg Leu Lys Ala Leu Ser Phe Leu Val			

165								170					175				
Leu	Leu	Glu	Asp	Glu	Ser	Thr	Pro	Cys	Glu	Val	Pro	His	Phe	Ala	Ser		
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Pro	Thr	Ala	Cys	Arg	Ala	Val	Ala	Ala	His	Gln	Leu	Phe	Asp	Ala	Ser		
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Gly	His	Gly	Leu	Asn	Glu	Ala	Asp	Ala	Asp	Phe	Leu	Asp	Asp	Leu	Leu		
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Ser	Arg	His	Val	Ile	Arg	Ala	Leu	Val	Gly	Glu	Arg	Gly	Ser	Ser	Ser		
								220						225			
Gly	Leu	Leu	Ser	Pro	Gln	Arg	Ala	Leu	Cys	Leu	Leu	Glu	Leu	Thr	Leu		
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Glu	His	Cys	Arg	Arg	Phe	Cys	Trp	Ser	Arg	His	His	Asp	Lys	Ala	Ile		
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Ser	Ala	Val	Glu	Lys	Ala	His	Ser	Tyr	Leu	Arg	Asn	Thr	Asn	Leu	Ala		
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Pro	Ser	Leu	Gln	Leu	Cys	Gln	Leu	Gly	Val	Lys	Leu	Leu	Gln	Val	Gly		
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Glu	Glu	Gly	Pro	Gln	Ala	Val	Ala	Lys	Leu	Leu	Ile	Lys	Ala	Ser	Ala		
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Val	Leu	Ser	Lys	Ser	Met	Glu	Ala	Pro	Ser	Pro	Pro	Leu	Arg	Ala	Leu		
								280						285			
Tyr	Glu	Ser	Cys	Gln	Phe	Phe	Leu	Ser	Gly	Leu	Glu	Arg	Gly	Thr	Lys		
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Arg	Arg	Tyr	Arg	Leu	Asp	Ala	Ile	Leu	Ser	Leu	Phe	Ala	Phe	Leu	Gly		
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Gly	Tyr	Cys	Ser	Leu	Leu	Gln	Gln	Leu	Arg	Asp	Asp	Gly	Val	Tyr	Gly		
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Gly	Ser	Ser	Lys	Gln	Gln	Gln	Ser	Phe	Leu	Gln	Met	Tyr	Phe	Gln	Gly		
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Leu	His	Leu	Tyr	Thr	Val	Val	Val	Tyr	Asp	Phe	Ala	Gln	Gly	Cys	Gln		
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Ile	Val	Asp	Leu	Ala	Asp	Leu	Thr	Gln	Leu	Val	Asp	Ser	Cys	Lys	Ser		
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Thr	Val	Val	Trp	Met	Leu	Glu	Ala	Leu	Glu	Gly	Leu	Ser	Gly	Gln	Glu		
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Leu	Thr	Asp	His	Met	Gly	Met	Thr	Ala	Ser	Tyr	Thr	Ser	Asn	Leu	Ala		
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Tyr	Ser	Phe	Tyr	Ser	His	Lys	Leu	Tyr	Ala	Glu	Ala	Cys	Ala	Ile	Ser		
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Glu	Pro	Leu	Cys	Gln	His	Leu	Gly	Leu	Val	Lys	Pro	Gly	Thr	Tyr	Pro		
								380						385			

Glu Val Pro Pro Glu Lys Leu His Arg Cys Phe Arg Leu Gln Val Glu  
 500 505 510  
 Ser Leu Lys Lys Leu Gly Lys Gln Ala Gln Gly Cys Lys Met Val Ile  
 515 520 525  
 Leu Trp Leu Ala Ala Leu Gln Pro Cys Ser Pro Glu His Met Ala Glu  
 530 535 540  
 Pro Val Thr Phe Trp Val Arg Val Lys Met Asp Ala Ala Arg Ala Gly  
 545 550 555 560  
 Asp Lys Glu Leu Gln Leu Lys Thr Leu Arg Asp Ser Leu Ser Gly Trp  
 565 570 575  
 Asp Pro Glu Thr Leu Ala Leu Leu Leu Arg Glu Glu Leu Gln Ala Tyr  
 580 585 590  
 Lys Ala Val Arg Ala Asp Thr Gly Gln Glu Arg Phe Asn Ile Ile Cys  
 595 600 605  
 Asp Leu Leu Glu Leu Ser Pro Glu Glu Thr Pro Ala Gly Ala Trp Ala  
 610 615 620  
 Arg Ala Thr His Leu Val Glu Leu Ala Gln Val Leu Cys Tyr His Asp  
 625 630 635 640  
 Phe Thr Gln Gln Thr Asn Cys Ser Ala Leu Asp Ala Ile Arg Glu Ala  
 645 650 655  
 Leu Gln Leu Leu Asp Ser Val Arg Pro Glu Ala Gln Ala Arg Asp Gln  
 660 665 670  
 Leu Leu Asp Asp Lys Ala Gln Ala Leu Leu Trp Leu Tyr Ile Cys Thr  
 675 680 685  
 Leu Glu Ala Lys Ile Gln Glu Gly Ile Glu Arg Asp Arg Arg Ala Gln  
 690 695 700  
 Ala Pro Gly Asn Leu Glu Glu Phe Glu Val Asn Asp Leu Asn Tyr Glu  
 705 710 715 720  
 Asp Lys Leu Gln Glu Asp Arg Phe Leu Tyr Ser Asn Ile Ala Phe Asn  
 725 730 735  
 Leu Ala Ala Asp Ala Ala Gln Ser Lys Cys Leu Asp Gln Ala Leu Ala  
 740 745 750  
 Leu Trp Lys Glu Leu Leu Thr Lys Gly Gln Ala Pro Ala Val Arg Cys  
 755 760 765  
 Leu Gln Gln Thr Ala Ala Ser Leu Gln Ile Leu Ala Ala Leu Tyr Gln  
 770 775 780  
 Leu Val Ala Lys Pro Met Gln Ala Leu Glu Val Leu Leu Leu Leu Arg  
 785 790 795 800  
 Ile Val Ser Glu Arg Leu Lys Asp His Ser Lys Ala Ala Gly Ser Ser  
 805 810 815  
 Cys His Ile Thr Gln Leu Leu Leu Thr Leu Gly Cys Pro Ser Tyr Ala  
 820 825 830

Gln Leu His Leu Glu Glu Ala Ala Ser Ser Leu Lys His Leu Asp Gln  
 835 840 845  
 Thr Thr Asp Thr Tyr Leu Leu Leu Ser Leu Thr Cys Asp Leu Leu Arg  
 850 855 860  
 Ser Gln Leu Tyr Trp Thr His Gln Lys Val Thr Lys Gly Val Ser Leu  
 865 870 875 880  
 Leu Leu Ser Val Leu Arg Asp Pro Ala Leu Gln Lys Ser Ser Lys Ala  
 885 890 895  
 Trp Tyr Leu Leu Arg Val Gln Val Leu Gln Leu Val Ala Ala Tyr Leu  
 900 905 910  
 Ser Leu Pro Ser Asn Asn Leu Ser His Ser Leu Trp Glu Gln Leu Cys  
 915 920 925  
 Ala Gln Gly Trp Gln Thr Pro Glu Ile Ala Leu Ile Asp Ser His Lys  
 930 935 940  
 Leu Leu Arg Ser Ile Ile Leu Leu Leu Met Gly Ser Asp Ile Leu Ser  
 945 950 955 960  
 Thr Gln Lys Ala Ala Val Glu Thr Ser Phe Leu Asp Tyr Gly Glu Asn  
 965 970 975  
 Leu Val Gln Lys Trp Gln Val Leu Ser Glu Val Leu Ser Cys Ser Glu  
 980 985 990  
 Lys Leu Val Cys His Leu Gly Arg Leu Gly Ser Val Ser Glu Ala Lys  
 995 1000 1005  
 Ala Phe Cys Leu Glu Ala Leu Lys Leu Thr Thr Lys Leu Gln Ile Pro  
 1010 1015 1020  
 Arg Gln Cys Ala Leu Phe Leu Val Leu Lys Gly Glu Leu Glu Leu Ala  
 1025 1030 1035 1040  
 Arg Asn Asp Ile Asp Leu Cys Gln Ser Asp Leu Gln Gln Val Leu Phe  
 1045 1050 1055  
 Leu Leu Glu Ser Cys Thr Glu Phe Gly Gly Val Thr Gln His Leu Asp  
 1060 1065 1070  
 Ser Val Lys Lys Val His Leu Gln Lys Gly Lys Gln Gln Ala Gln Val  
 1075 1080 1085  
 Pro Cys Pro Pro Gln Leu Pro Glu Glu Glu Leu Phe Leu Arg Gly Pro  
 1090 1095 1100  
 Ala Leu Glu Leu Val Ala Thr Val Ala Lys Glu Pro Gly Pro Ile Ala  
 1105 1110 1115 1120  
 Pro Ser Thr Asn Ser Ser Pro Val Leu Lys Thr Lys Pro Gln Pro Ile  
 1125 1130 1135  
 Pro Asn Phe Leu Ser His Ser Pro Thr Cys Asp Cys Ser Leu Cys Ala  
 1140 1145 1150  
 Ser Pro Val Leu Thr Ala Val Cys Leu Arg Trp Val Leu Val Thr Ala

1155	1160	1165
Gly Val Arg Leu Ala Met Gly His Gln Ala Gln Gly Leu Asp Leu Leu 1170 1175 1180		
Gln Val Val Leu Lys Gly Cys Pro Glu Ala Ala Glu Arg Leu Thr Gln 1185 1190 1195 1200		
Ala Leu Gln Ala Ser Leu Asn His Lys Thr Pro Pro Ser Leu Val Pro 1205 1210 1215		
Ser Leu Leu Asp Glu Ile Leu Ala Gln Ala Tyr Thr Leu Leu Ala Leu 1220 1225 1230		
Glu Gly Leu Asn Gln Pro Ser Asn Glu Ser Leu Gln Lys Val Leu Gln 1235 1240 1245		
Ser Gly Leu Lys Phe Val Ala Ala Arg Ile Pro His Leu Glu Pro Trp 1250 1255 1260		
Arg Ala Ser Leu Leu Leu Ile Trp Ala Leu Thr Lys Leu Gly Gly Leu 1265 1270 1275 1280		
Ser Cys Cys Thr Thr Gln Leu Phe Ala Ser Ser Trp Gly Trp Gln Pro 1285 1290 1295		
Pro Leu Ile Lys Ser Val Pro Gly Ser Glu Pro Ser Lys Thr Gln Gly 1300 1305 1310		
Gln Lys Arg Ser Gly Arg Gly Arg Gln Lys Leu Ala Ser Ala Pro Leu 1315 1320 1325		
Ser Leu Asn Asn Thr Ser Gln Lys Gly Leu Glu Gly Arg Gly Leu Pro 1330 1335 1340		
Cys Thr Pro Lys Pro Pro Asp Arg Ile Arg Gln Ala Gly Pro His Val 1345 1350 1355 1360		
Pro Phe Thr Val Phe Glu Glu Val Cys Pro Thr Glu Ser Lys Pro Glu 1365 1370 1375		
Val Pro Gln Ala Pro Arg Val Gln Gln Arg Val Gln Thr Arg Leu Lys 1380 1385 1390		
Val Asn Phe Ser Asp Asp Ser Asp Leu Glu Asp Pro Val Ser Ala Glu 1395 1400 1405		
Ala Trp Leu Ala Glu Glu Pro Lys Arg Arg Gly Thr Ala Ser Arg Gly 1410 1415 1420		
Arg Gly Arg Ala Arg Lys Gly Leu Ser Leu Lys Thr Asp Ala Val Val 1425 1430 1435 1440		
Ala Pro Gly Ser Ala Pro Gly Asn Pro Gly Leu Asn Gly Arg Ser Arg 1445 1450 1455		
Arg Ala Lys Lys Val Ala Ser Arg His Cys Glu Glu Arg Arg Pro Gln 1460 1465 1470		
Arg Ala Ser Asp Gln Ala Arg Pro Gly Pro Glu Ile Met Arg Thr Ile 1475 1480 1485		
Pro Glu Glu Glu Leu Thr Asp Asn Trp Arg Lys Met Ser Phe Glu Ile		

1490	1495	1500
Leu Arg Gly Ser Asp 1505	Gly Glu Asp Ser Ala 1510	Ser Gly Gly Lys Thr Pro 1515 1520
Ala Pro Gly Pro Glu 1525	Ala Ala Ser Gly Glu 1530	Trp Glu Leu Leu Arg Leu 1535
Asp Ser Ser Lys Lys 1540	Lys Leu Pro Ser Pro 1545	Cys Pro Asp Lys Glu Ser 1550
Asp Lys Asp Leu Gly 1555	Pro Arg Leu Gln Leu 1560	Pro Ser Ala Pro Val Ala 1565
Thr Gly Leu Ser Thr 1570	Leu Asp Ser Ile Cys 1575	Asp Ser Leu Ser Val Ala 1580
Phe Arg Gly Ile Ser 1585	His Cys Pro Pro Ser 1590 1595	Gly Leu Tyr Ala His Leu 1600
Cys Arg Phe Leu Ala 1605	Leu Cys Leu Gly His 1610	Arg Asp Pro Tyr Ala Thr 1615
Ala Phe Leu Val Thr 1620	Glu Ser Val Ser Ile 1625	Thr Cys Arg His Gln Leu 1630
Leu Thr His Leu His 1635	Arg Gln Leu Ser Lys 1640	Ala Gln Lys His Arg Gly 1645
Ser Leu Glu Ile Ala 1650	Asp Gln Leu Gln Gly 1655	Leu Ser Leu Gln Glu Met 1660
Pro Gly Asp Val Pro 1665	Leu Ala Arg Ile Gln 1670	Arg Leu Phe Ser Phe Arg 1675 1680
Ala Leu Glu Ser Gly 1685	His Phe Pro Gln Pro 1690	Glu Lys Glu Ser Phe Gln 1695
Glu Arg Leu Ala Leu 1700	Ile Pro Ser Gly Val 1705	Thr Val Cys Val Leu Ala 1710
Leu Ala Thr Leu Gln 1715	Pro Gly Thr Val Gly 1720	Asn Thr Leu Leu Thr 1725
Arg Leu Glu Lys Asp 1730	Ser Pro Pro Val Ser 1735	Val Gln Ile Pro Thr Gly 1740
Gln Asn Lys Leu His 1745	Leu Arg Ser Val Leu 1750	Asn Glu Phe Asp Ala Ile 1755 1760
Gln Lys Ala Gln Lys 1765	Glu Asn Ser Ser Cys 1770	Thr Asp Lys Arg Glu Trp 1775
Trp Thr Gly Arg Leu 1780	Ala Leu Asp His Arg 1785	Met Glu Val Leu Ile Ala 1790
Ser Leu Glu Lys Ser 1795	Val Leu Gly Cys Trp 1800	Lys Gly Leu Leu Leu Pro 1805
Ser Ser Glu Glu Pro 1810	Gly Pro Ala Gln Glu 1815	Ala Ser Arg Leu Gln Glu 1820

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 1825 1830 1835 1840  
 Ile Met Leu Ser Gly Ala Gly Ala Leu Thr Pro Gln Asp Ile Gln Ala  
 1845 1850 1855  
 Leu Ala Tyr Gly Leu Cys Pro Thr Gln Pro Glu Arg Ala Gln Glu Leu  
 1860 1865 1870  
 Leu Asn Glu Ala Val Gly Arg Leu Gln Gly Leu Thr Val Pro Ser Asn  
 1875 1880 1885  
 Ser His Leu Val Leu Val Leu Asp Lys Asp Leu Gln Lys Leu Pro Trp  
 1890 1895 1900  
 Glu Ser Met Pro Ser Leu Gln Ala Leu Pro Val Thr Arg Leu Pro Ser  
 1905 1910 1915 1920  
 Phe Arg Phe Leu Leu Ser Tyr Ser Ile Ile Lys Glu Tyr Gly Ala Ser  
 1925 1930 1935  
 Pro Val Leu Ser Gln Gly Val Asp Pro Arg Ser Thr Phe Tyr Val Leu  
 1940 1945 1950  
 Asn Pro His Asn Asn Leu Ser Ser Thr Glu Glu Gln Phe Arg Ala Asn  
 1955 1960 1965  
 Phe Ser Ser Glu Ala Gly Trp Arg Gly Val Val Gly Glu Val Pro Arg  
 1970 1975 1980  
 Pro Glu Gln Val Gln Glu Ala Leu Thr Lys His Asp Leu Tyr Ile Tyr  
 1985 1990 1995 2000  
 Ala Gly His Gly Ala Gly Ala Arg Phe Leu Asp Gly Gln Ala Val Leu  
 2005 2010 2015  
 Arg Leu Ser Cys Arg Ala Val Ala Leu Leu Phe Gly Cys Ser Ser Ala  
 2020 2025 2030  
 Ala Leu Ala Val His Gly Asn Leu Glu Gly Ala Gly Ile Val Leu Lys  
 2035 2040 2045  
 Tyr Ile Met Ala Gly Cys Pro Leu Phe Leu Gly Asn Leu Trp Asp Val  
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 Thr Asp Arg Asp Ile Asp Arg Tyr Thr Glu Ala Leu Leu Gln Gly Trp  
 2065 2070 2075 2080  
 Leu Gly Ala Gly Pro Gly Ala Pro Leu Leu Tyr Tyr Val Asn Gln Ala  
 2085 2090 2095



Arg Gln Ala Pro Arg Leu Lys Tyr Leu Ile Gly Ala Ala Pro Ile Ala  
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Tyr Gly Leu Pro Val Ser Leu Arg  
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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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24

<210> 5

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 5

gaattcta at acgactcact ataggatcca tgatccctga ggaagaactg actg

54

<210> 6

<211> 55

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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55

<210> 7

<211> 56

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: primer

&lt;400&gt; 7

gaattctaatac gactcact ataggatcca tggattccag caagaagaag ctgccc 56

&lt;210&gt; 8

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: primer

&lt;400&gt; 8

ttattaccgc agagagacag gcaagcc 27

&lt;210&gt; 9

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (6)...(6)

&lt;223&gt; 7-Amido-4-methylcoumarin

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: recognition site

&lt;400&gt; 9

Asp Arg Glu Ile Met Arg

1

5

&lt;210&gt; 10

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: peptide inhibitor

&lt;400&gt; 10

Ser Val Glu Gln Gly Arg

1

5

&lt;210&gt; 11

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (6)...(6)

&lt;223&gt; 7-Amido-4-methylcoumarin

<220>

<223> Description of Artificial Sequence: recognition site

<400> 11

Ser Phe Glu Ile Leu Arg  
1 5

<210> 12

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> MOD\_RES

<222> (6)...(6)

<223> 7-Amido-4-methylcoumarin

<220>

<223> Description of Artificial Sequence: peptide inhibitor

<400> 12

Glu Trp Glu Leu Leu Arg  
1 5

<210> 13

<211> 7

<212> PRT

<213> Artificial Sequence

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<221> MOD\_RES

<222> (7)...(7)

<223> 7-Amido-4-methylcoumarin

<220>

<221> Description of Artificial Sequence: recognition site

<400> 13

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1 5